multi - french

Imperial College

load data

```
# from https://www.data.gouv.fr/fr/datasets/donnees-de-laboratoires-pour-le-depistage-indicateurs-sur-l

d <- read.csv(file = 'Rdata/sp-variant-7j-reg-2021-06-02-21h05.csv',sep=';')
d$reg <- as.character(d$reg)
d$cl_age90 <- as.character(d$cl_age90)
unique(d$cl_age90)
```

```
##  [1] "9"  "19" "29" "39" "49" "59" "69" "79" "89" "90" "0"
```

```
d$week_end <- as.Date(substr(d$semaine, 1, 10),format = '%Y-%m-%d')+6

# rename regions
f <- which(d$reg %in% c('5','7','8'))
d <- d[-f,]

# from
d_region <- read.csv(file = 'Rdata/regions-france.csv',encoding = "UTF-8")
d$region <- as.character(d_region$nom_region[match(d$reg,d_region$code_region)])
# unique(d$region)
# unique(d_region$code_region)
# sort(unique(d$reg))

# rename variants
variants0 <- c('Nb_susp_ABS','Nb_susp_501Y_V1','Nb_susp_501Y_V2_3')
# match(variants,names(d))
variants <- c('wild','alpha','beta/gamma')

names(d) [match(variants0,names(d))]<- variants
```

get list of matrix, 1 for each variant with 1 column for dates and 'n' columns for each location

```
# for incidence
regions <- sort(unique(d$reg))
#for Rt
mean_prior <- c(2)
std_prior <- c(1)
#
mean_SI <- 5.4 # mean 5.4 days and standard deviation of 1.5 days (Rai, Shukla, and Dwivedi 2021).
std_SI <- 1.5
SI_assumed <- EpiEstim::discr_si(seq(0, 20), mean_SI, std_SI)
t_window <- 7
n_sample_R <- 1e1
```

```
u_age <- unique(d$cl_age90)

initial_res <- wrapper(age_group = u_age[11] , regions = regions, plot_incidence = FALSE,
                       variants = variants, t_window = t_window,
                       SI = SI_assumed, mean_prior = mean_prior,
                       std_prior = std_prior, n_sample_R = n_sample_R, plot_Rt = FALSE)
```

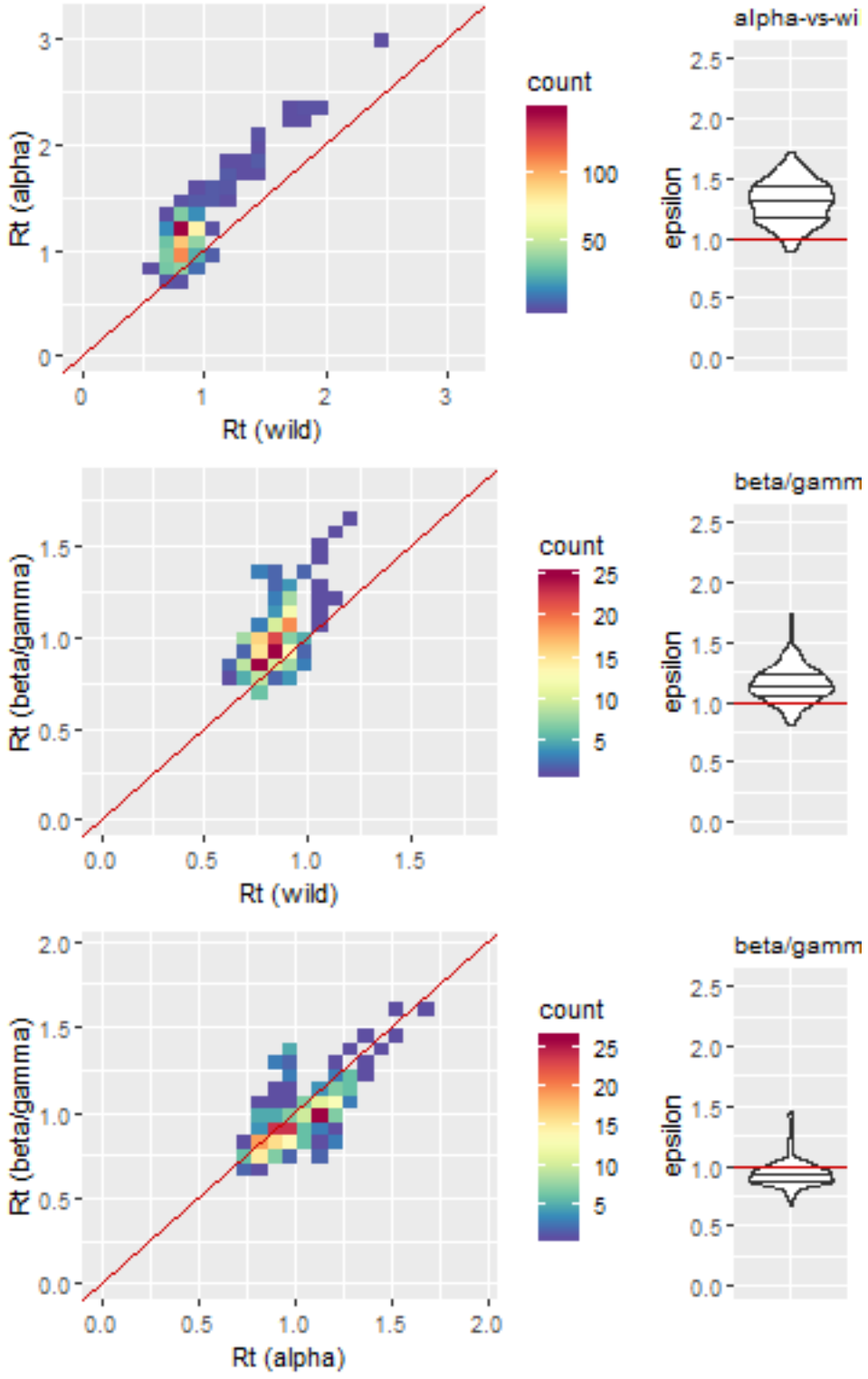
table looking at inclusion

days where 2 variants have Rt estimates with 95%CrI lower than 0.5

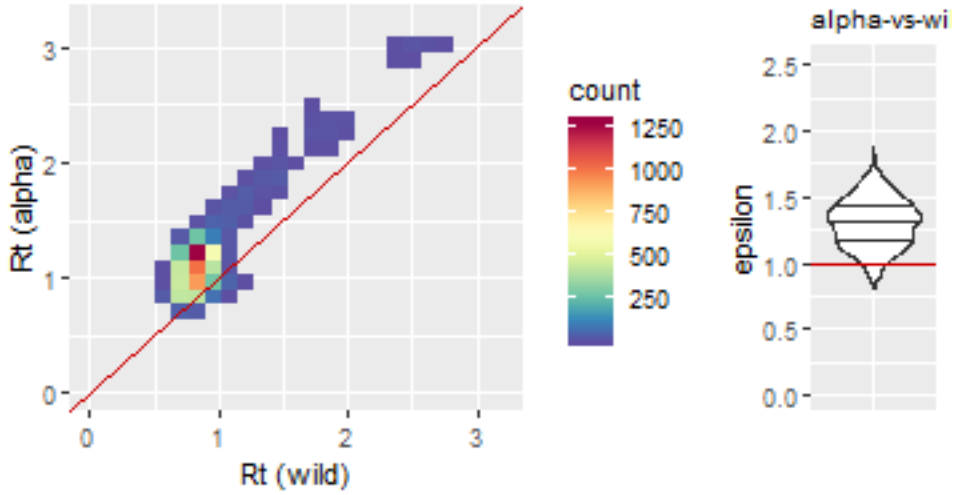
```
selection <- select_Rt_get_median_samples(th = 0.2, # only keep where 95%CrI of Rt less then 0.2
                                          EpiEstim_Rt = initial_res$EpiEstim_Rt,
                                          regions = regions,
                                          variants = variants,
                                          SI = SI_assumed,
                                          trim = 0)


selection$summary_select
```

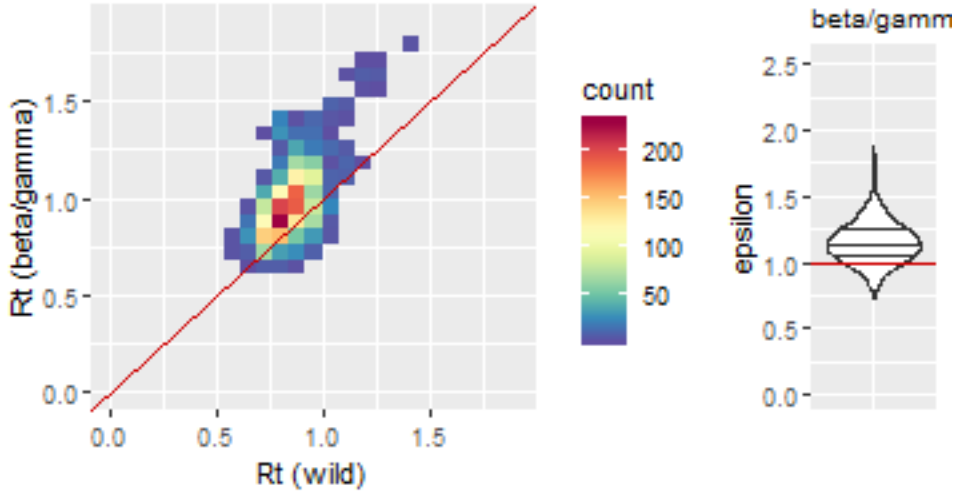
```
##    region wild-vs-alpha wild-vs-beta/gamma alpha-vs-beta/gamma
## 1       1            73                 46                  46
## 2      11            58                  3                   3
## 3       2            27                  0                   0
## 4      24            44                  0                   0
## 5      27             0                  0                   0
## 6      28            75                 74                  91
## 7       3             0                  0                   0
## 8      32             0                  0                   0
## 9       4            75                 16                  16
## 10     44            95                 92                  92
## 11     52             0                  0                   0
## 12     53             0                  0                   0
## 13      6             0                  0                   0
## 14     75            56                  0                   0
## 15     76            57                  0                   0
## 16     84            70                  1                   1
## 17     93            66                 27                  32
## 18     94            67                 22                  24
```

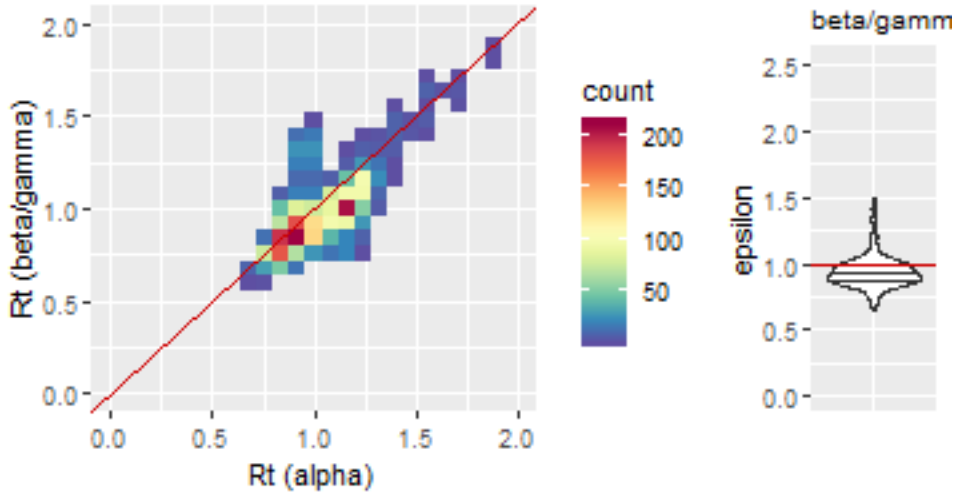
```
plot_hist_dist(x = selection$median_Rts, x_sum = selection$summary_select)
```




```
plot_hist_dist(x = selection$samples_Rts, x_sum = selection$summary_select)
```





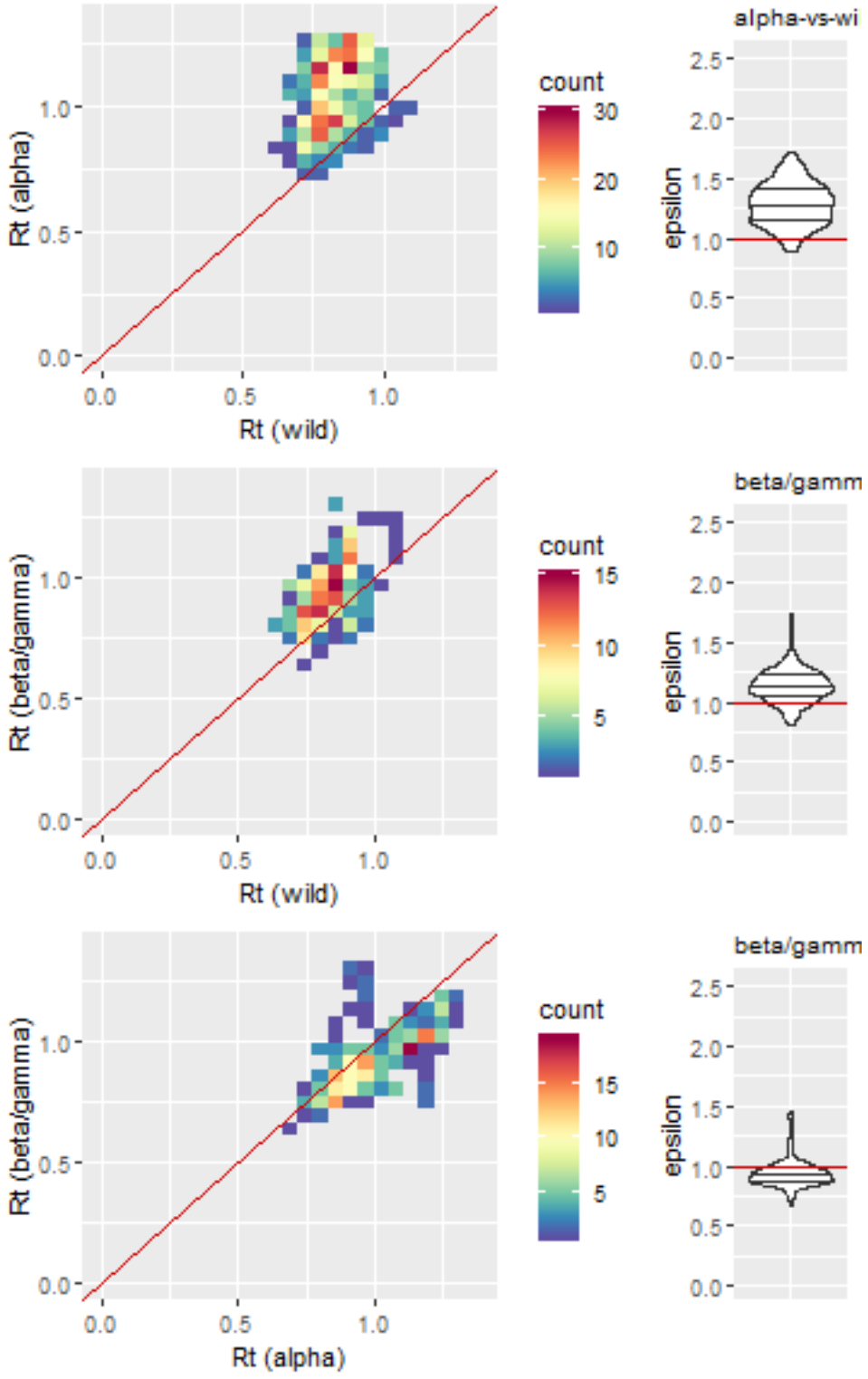



```
# second
selection <- select_Rt_get_median_samples(th = 0.2,
                                          EpiEstim_Rt = initial_res$EpiEstim_Rt,
                                          regions = regions,
                                          variants = variants,
```

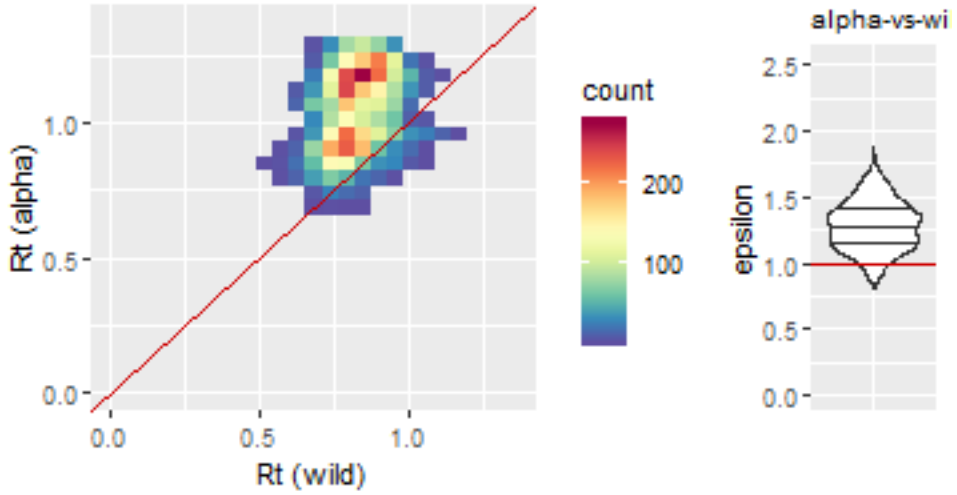
```
                                        SI = SI_assumed,
                                        trim = 0.99) # trim initial Rt until cumsum(1:x)>=0.99
selection$summary_select
```

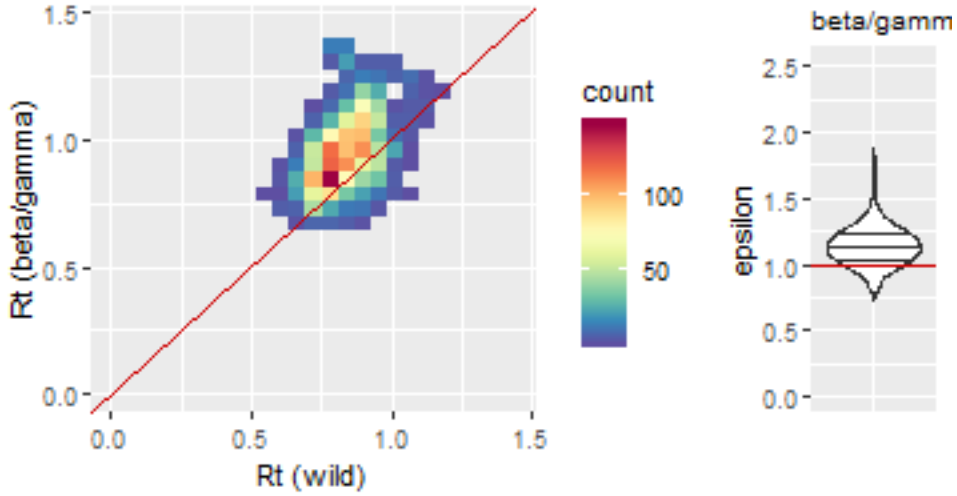
```
##    region wild-vs-alpha wild-vs-beta/gamma alpha-vs-beta/gamma
## 1       1            63                 46                  46
## 2      11            51                  3                   3
## 3       2            19                  0                   0
## 4      24            37                  0                   0
## 5      27             0                  0                   0
## 6      28            66                 66                  83
## 7       3             0                  0                   0
## 8      32             0                  0                   0
## 9       4            65                 16                  16
## 10     44            85                 85                  85
## 11     52             0                  0                   0
## 12     53             0                  0                   0
## 13      6             0                  0                   0
## 14     75            48                  0                   0
## 15     76            49                  0                   0
## 16     84            60                  1                   1
## 17     93            57                 27                  32
## 18     94            57                 21                  23
```

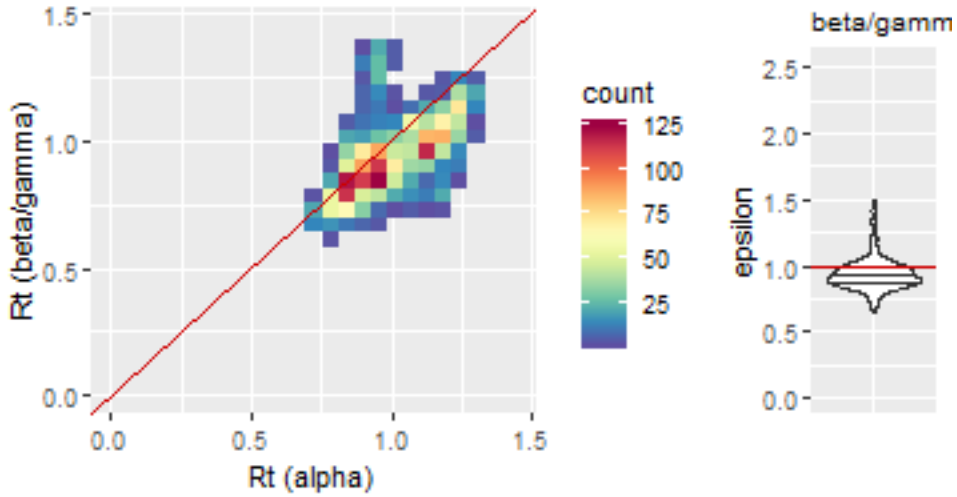
```
plot_hist_dist(x = selection$median_Rts, x_sum = selection$summary_select)
```




```
ep <- plot_hist_dist(x = selection$samples_Rts, x_sum = selection$summary_select, keep=TRUE)
```








```
res_epsi <- data.frame(matrix(NA,ncol = 4, nrow = length(u_age) ))
names(res_epsi) <- c('Age_class', names(ep))
res_epsi$Age_class <- u_age

for(i in 1:3){
```

```
  temp <- round(quantile(ep[[i]],c(0.5,.025,.975)),digits = 2)
  res_epsi[length(u_age),1+i] <- paste0(temp[1],' ; 95%CrI[',temp[2],' ; ',temp[3],']')
}
```

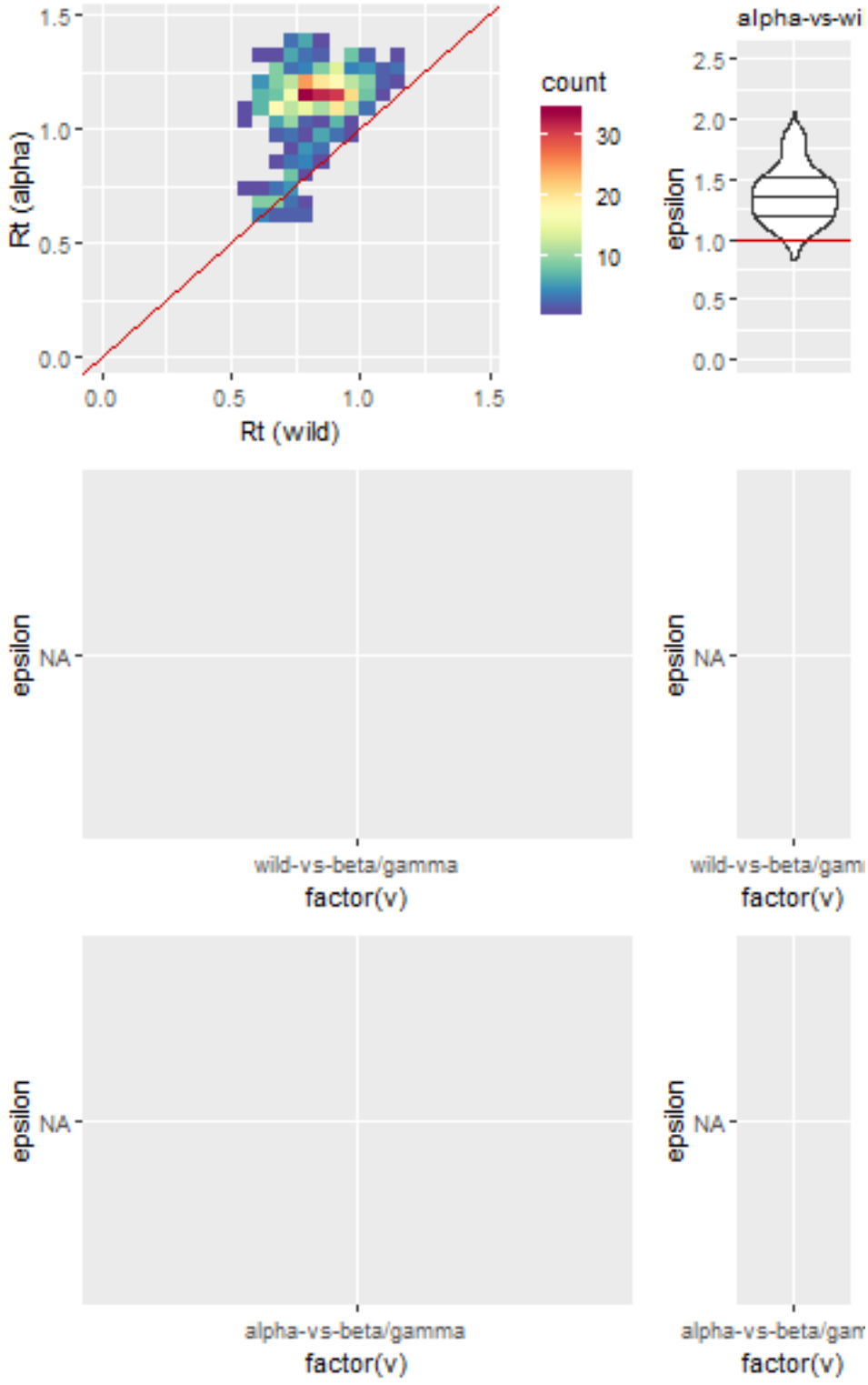
for 0-9

```
for(j in 1:(length(u_age)-1)){
  print(u_age[j])

  initial_res <- wrapper(age_group = u_age[j], regions = regions, plot_incidence = FALSE,
                         variants = variants, t_window = t_window,
                         SI = SI_assumed, mean_prior = mean_prior,
                         std_prior = std_prior, n_sample_R = n_sample_R, plot_Rt = FALSE)

  selection <- select_Rt_get_median_samples(th = 0.2,
                                            EpiEstim_Rt = initial_res$EpiEstim_Rt,
                                            regions = regions,
                                            variants = variants,
                                            SI = SI_assumed,
                                            trim = 0.99)
  selection$summary_select


  ep <- plot_hist_dist(x = selection$samples_Rts, x_sum = selection$summary_select, keep=TRUE)

  for(i in 1:3){
    temp <- round(quantile(ep[[i]],c(0.5,.025,.975),na.rm=TRUE),digits = 2)
    res_epsi[j,1+i] <- paste0(temp[1],' ; 95%CrI[',temp[2],' ; ',temp[3],']')
  }

}
```

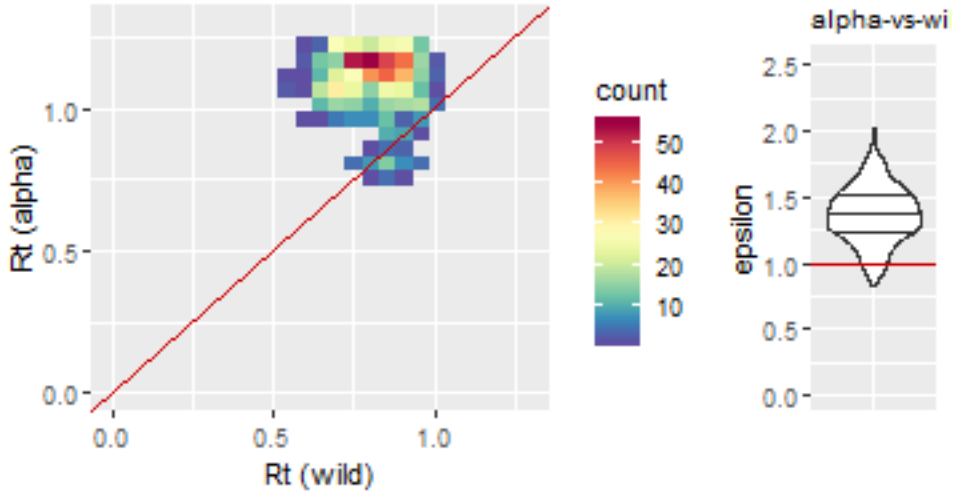
```
## [1] "9"
```

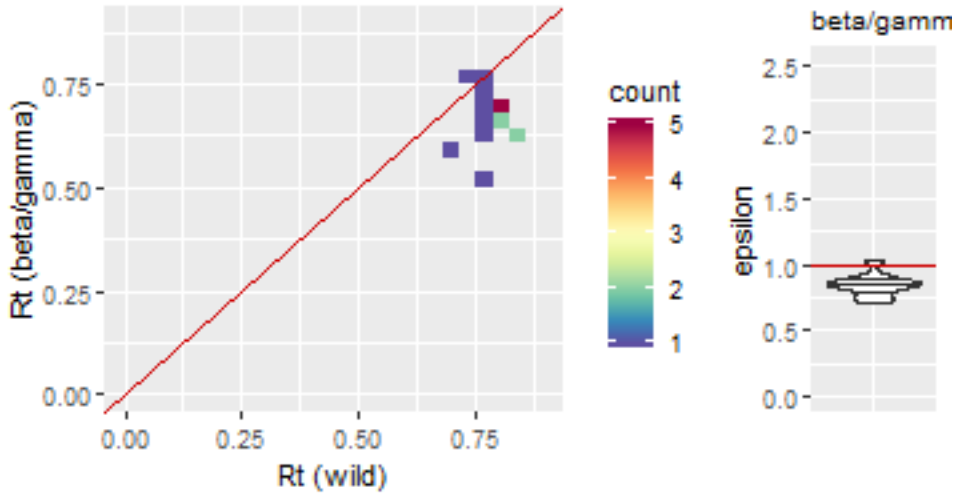

epsilon
NA
wild-vs-alpha
factor(v)
epsilon
NA
wild-vs-alpha
factor(v)
epsilon
NA
wild-vs-beta/gamma
factor(v)
epsilon
NA
wild-vs-beta/gam
factor(v)
epsilon
NA
alpha-vs-beta/gamma
factor(v)
epsilon
NA
alpha-vs-beta/gam
factor(v)

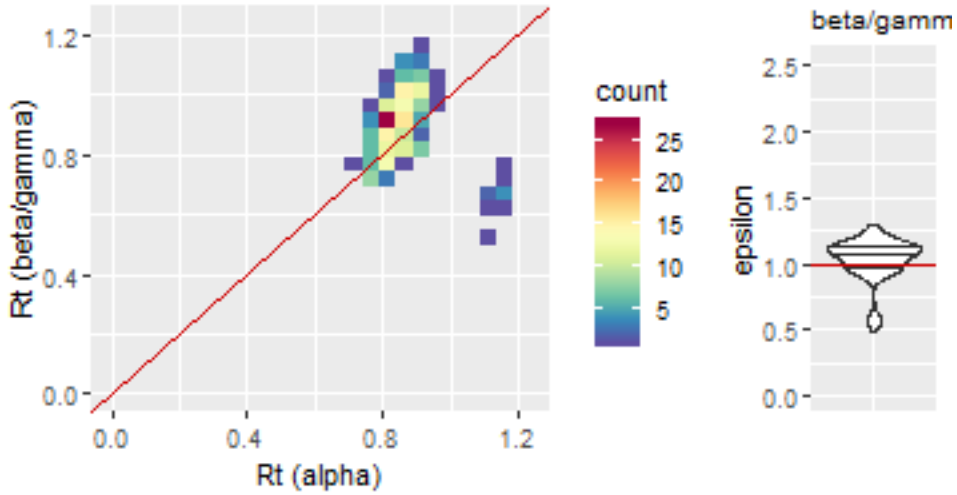
```
## [1] "19"
```


Rt (alpha)
Rt (wild)
count
30
20
10
alpha-vs-wi
epsilon
factor(v)
wild-vs-beta/gamma
alpha-vs-beta/gamma

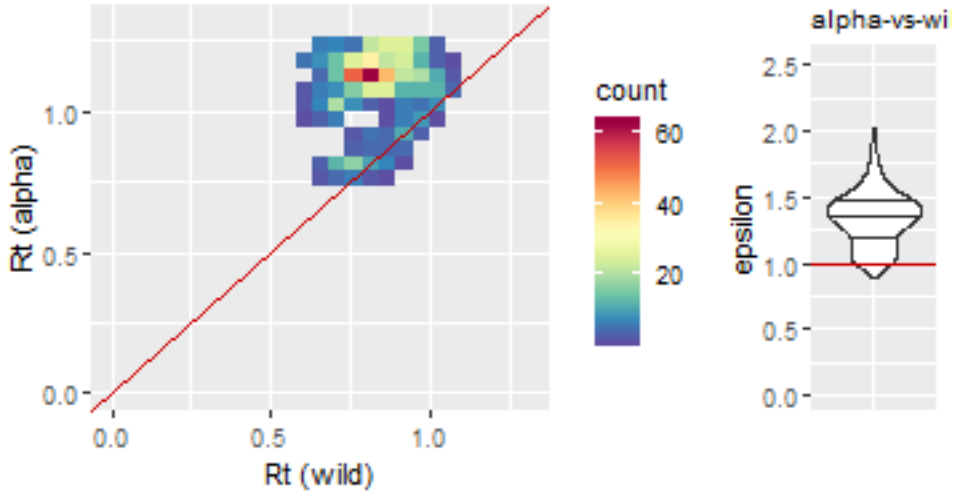
```
## [1] "29"
```

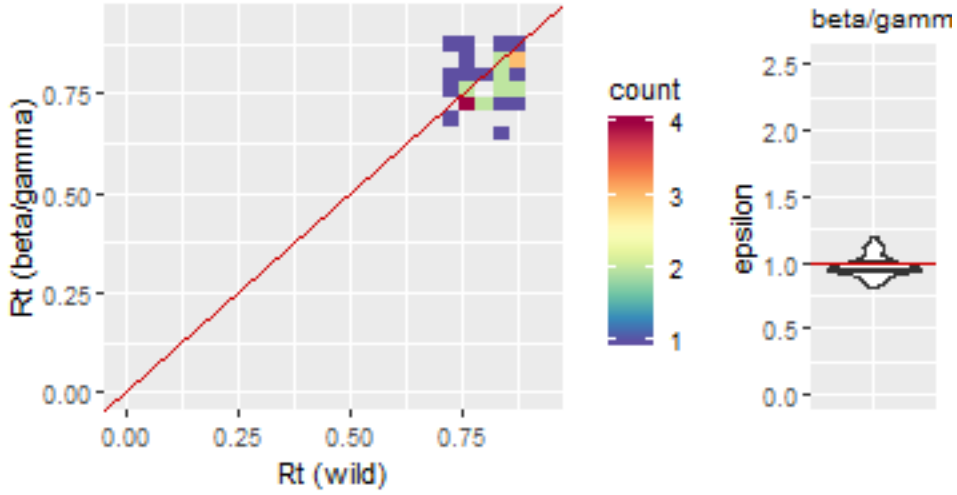

Rt (alpha)
Rt (wild)
count
50
40
30
20
10
alpha-vs-wi
epsilon

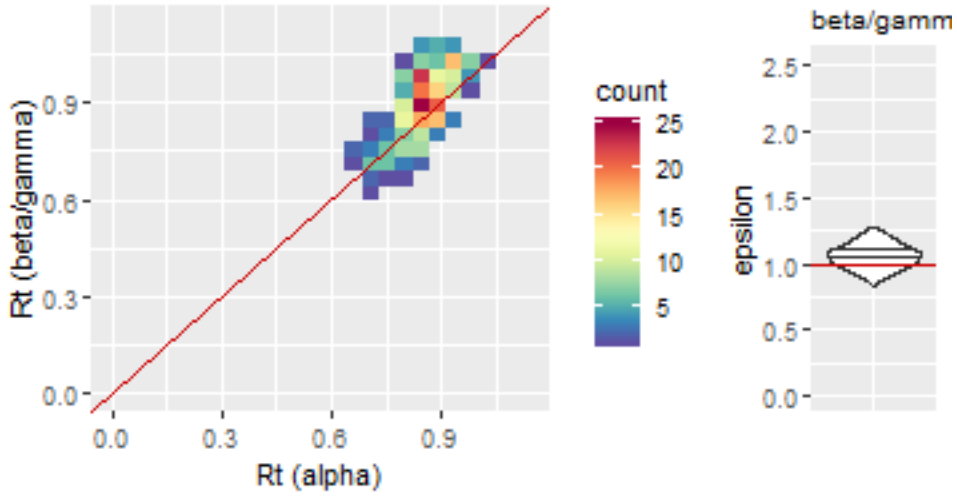

Rt (beta/gamma)
Rt (wild)
count
5
4
3
2
1
beta/gamm
epsilon


Rt (beta/gamma)
Rt (alpha)
count
25
20
15
10
5
beta/gamm
epsilon

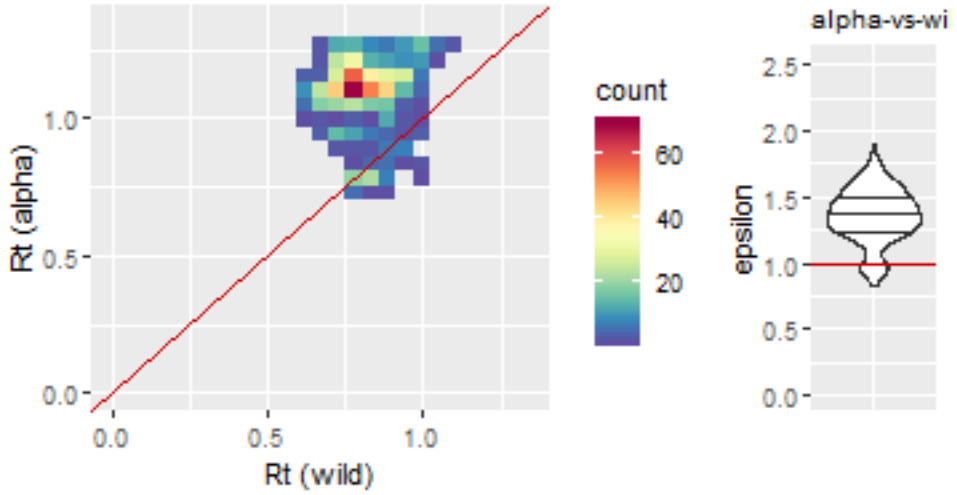
```
## [1] "39"
```

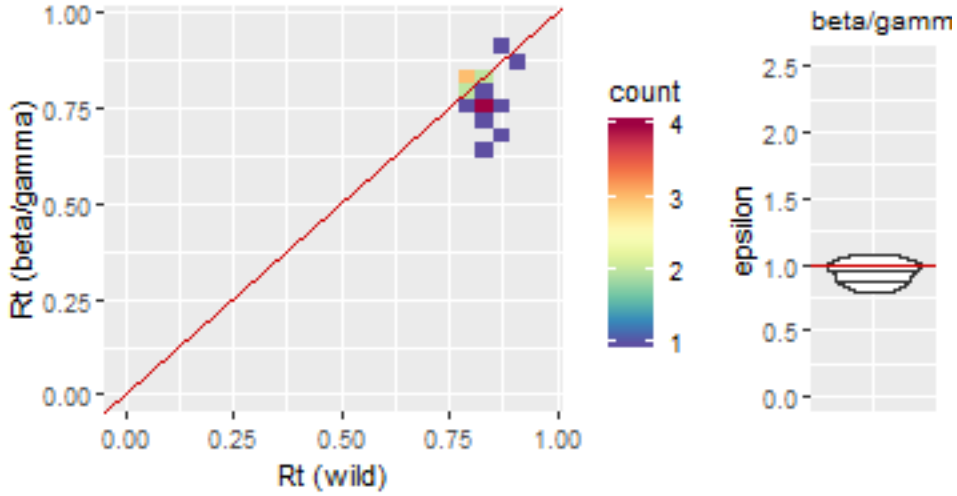

Rt (alpha)
Rt (wild)
count
60
40
20
alpha-vs-wi
epsilon

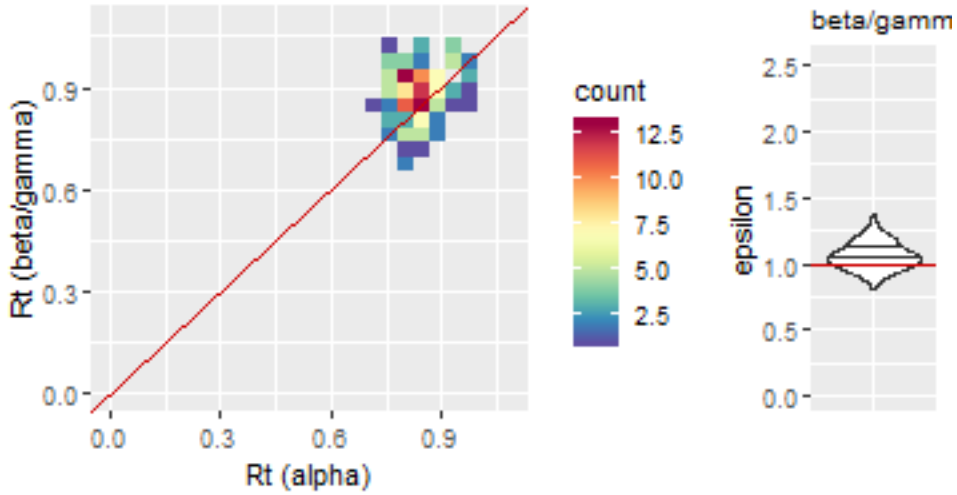

Rt (beta/gamma)
Rt (wild)
count
4
3
2
1
beta/gamm
epsilon


Rt (beta/gamma)
Rt (alpha)
count
25
20
15
10
5
beta/gamm
epsilon

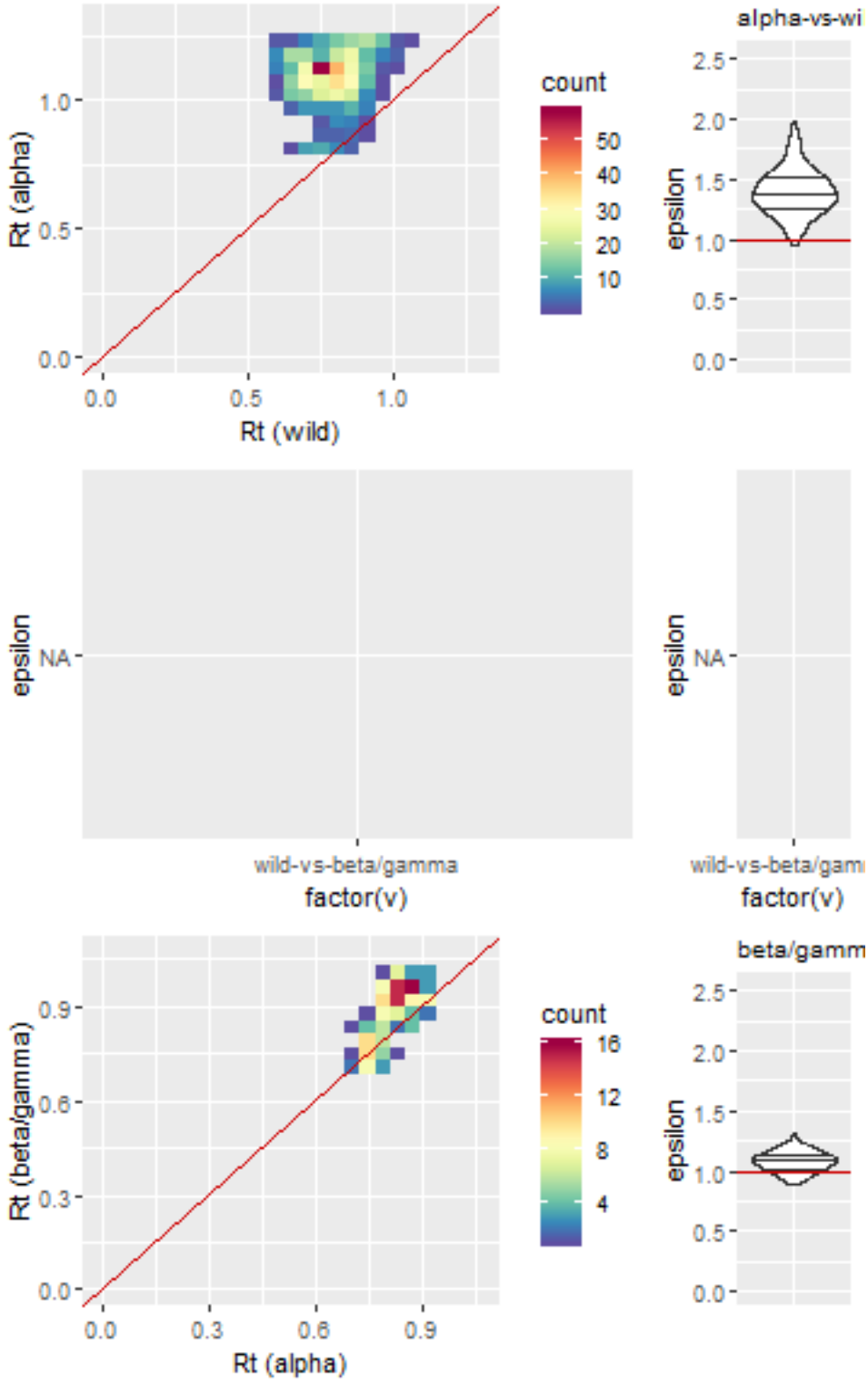
```
## [1] "49"
```


Rt (alpha)
Rt (wild)
count
60
40
20
alpha-vs-wi
epsilon
2.5
2.0
1.5
1.0
0.5
0.0

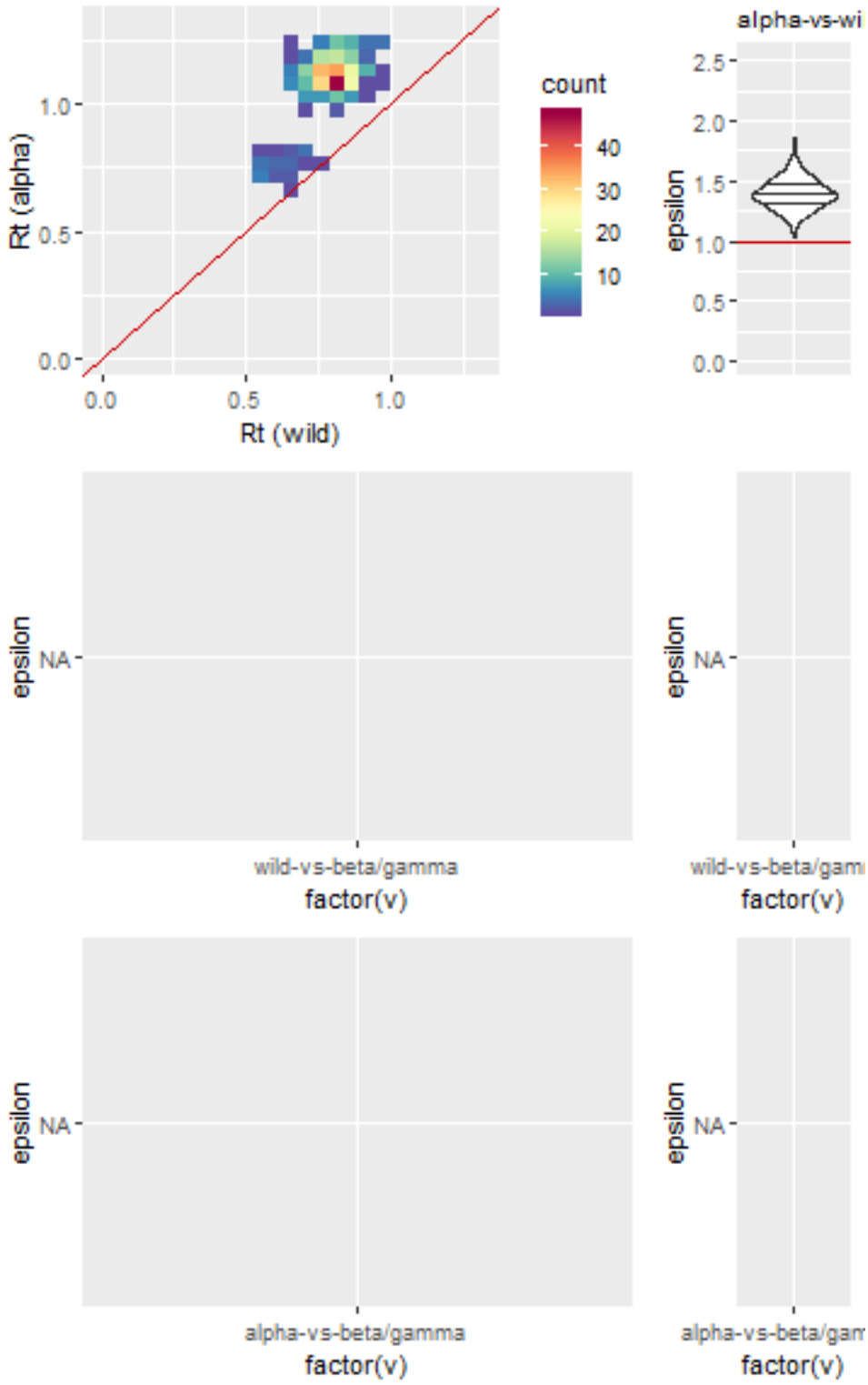

Rt (beta/gamma)
Rt (wild)
count
4
3
2
1
beta/gamm
epsilon
1.00
0.75
0.50
0.25
0.00


Rt (beta/gamma)
Rt (alpha)
count
12.5
10.0
7.5
5.0
2.5
beta/gamm
epsilon
0.9
0.6
0.3
0.0

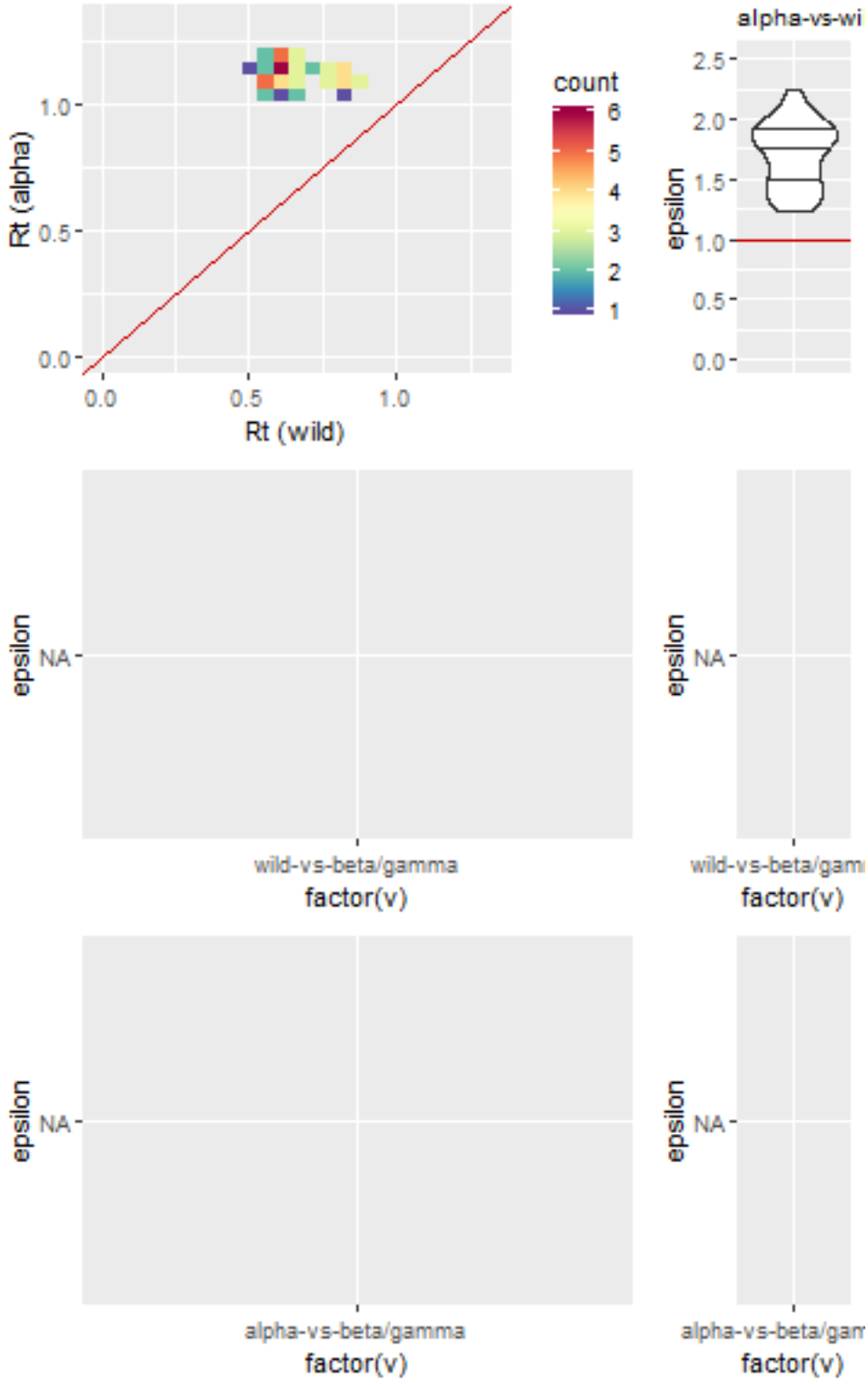
```
## [1] "59"
```


Rt (alpha)
Rt (wild)
count
50
40
30
20
10
alpha-vs-wi
epsilon
NA
wild-vs-beta/gamma
wild-vs-beta/gam
factor(v)
Rt (beta/gamma)
Rt (alpha)
16
12
8
4
beta/gamm

```
## [1] "69"
```


Rt (alpha)
Rt (wild)
0.0
0.5
1.0
count
40
30
20
10
alpha-vs-wi
epsilon
2.5
2.0
1.5
1.0
0.5
0.0
NA
wild-vs-beta/gamma
wild-vs-beta/gam
factor(v)
alpha-vs-beta/gamma
alpha-vs-beta/gam

```
## [1] "79"
```


Rt (alpha)
Rt (wild)
0.0
0.5
1.0
count
6
5
4
3
2
1
alpha-vs-wi
epsilon
2.5
2.0
1.5
1.0
0.5
0.0
NA
wild-vs-beta/gamma
wild-vs-beta/gam
alpha-vs-beta/gamma
alpha-vs-beta/gam
factor(v)

```
## [1] "89"
```


epsilon
NA
wild-vs-alpha
factor(v)
epsilon
NA
wild-vs-alpha
factor(v)
epsilon
NA
wild-vs-beta/gamma
factor(v)
epsilon
NA
wild-vs-beta/gam
factor(v)
epsilon
NA
alpha-vs-beta/gamma
factor(v)
epsilon
NA
alpha-vs-beta/gam
factor(v)

```
## [1] "90"
```


epsilon
NA
wild-vs-alpha
factor(v)
epsilon
NA
wild-vs-alpha
factor(v)
epsilon
NA
wild-vs-beta/gamma
factor(v)
epsilon
NA
wild-vs-beta/gam
factor(v)
epsilon
NA
alpha-vs-beta/gamma
factor(v)
epsilon
NA
alpha-vs-beta/gam
factor(v)